

1 TCGGTGCGCTGAGAGGTATCACCTCTTCTGGGCTCAAGATGGACAACAAGAAGCGCTGGCCTACGCCATCATCCAGTTCTGTCATGACCAGCTCCGGCA
M D N K K R L A Y A I I Q F L H D Q L R H>

101 CGGGGGCCTCTCGTCCGATGCTCAGGAGAGCTTGAAGTCCCATCCAGTGCCTGGAGACTGCGTTTGGGTGACGGTAGAAGACAGTGACCTTTCGGCTC
G G L S S D A O E S L E V A I O C L E T A F G V T V E D S D L A L >

201 CCTCAGACTCTGCGCGGAGATATTTGAAGCGGCTGCCACGGCAAGAGATGCCGAGGACCTGAGGAGCCCCAGCGCAACCCCGCTTCCGAGGAGGACT
P Q T L P E I F E A A A T G K E M P Q D L R S P A R T P P S E E D S>

301 CAGCAGAGCGCAGAGCGCCTCAAAACCGAAGGAAACGAGCAGATGAAGTGGAAACCTTTGAAGCTGCCGTGCATTTCTACGGAAGCCATCGAGCTCAA
A E A E R L K T E G N E O M K V E N F E A A V H F Y G K A I E L N>

401 CCCAGCCAAACGCGCTCTATTTCTGCAACAGAGCCGAGCCTACAGCAAACTCGGCAACTACGCGGCGCGTGCAGGACTGTGAGCGGGCCATCTGCATT
P A N A V Y F C N R A A A Y S K L G N Y A G A V O D C E R A I C I >

501 GACCGGCTTACAGCAAGGCTACGGCAGGATGGGCTCTCCAGCCTCAACAAGCACGTCGGAGCGCGTGGCTTACTACAAGAGCGCTGGAGC
D P A Y S K A Y G R M G L A L S S L N K H V E A V A Y Y K K A L E L>

601 TGGACCCCGACAACGAGACATACAAGTCCAACCTCAAGATAGCGGAGCTGAAGCTGCGGGAGGCCCCAGCCACGGGAGGCGTGGCAGCTTCGACAT
D P D N E T Y K S N L K I A E L K L R E A P S P T G G V G S F D I>

701 CGCGGCGCTGCTGAACAACCTGGCTTCATGAGCATGGCTTCGAACCTAATGAACAATCCCCAGATTTCAGCAGCTCATGTCCGGCATGATTTCCGGTGGC
A G L L N N P G F M S M A S N L M N N P Q I Q Q L M S G M I S G G >

801 AACAAACCCCTTGGGAACCTCCCGGACCCCTCGCAGAACGACCTGGCCAGCCTCATCCAGGCGGCGCAGCAGTTTTCGCCAGCAGATGCAGCAGCAGA
N N P L G T P G T S P S Q N D L A S L I Q A G Q Q Q F A Q Q M Q Q Q N>

FIG. 1A

901 ACCACAGTTGATAGAGCAGCTCAGGAGCCAAATCCGGAGTCGGACGCCAGCCAGCAACGACAGCAGGAGTGACGCTGCTCCTGCTCCCGGTGTGA
P E L I E Q L R S Q S G V G R P A P A T T S R S D A A C S R C D >

1001 CCGGTCCTTCCCTGGCCGACCCGGAAGCCTTCTGGTTGTCTGCCACTTCTCCTCTGTTGGACTGCCTGAGAGAGGGGAAGAGAGACCTCGGACCT
R V L P W P T R R K P S G C L P L P P V G L P E R G E R D L G P >

1101 GCATGTCAGATGGAATTTCCCTTTTATCTCTGCCCTGCTCCACTCCCTTTTGTAACTCCCTTACAGCCCCCAGACCTTCTTTGAAACGAGAGCCAGC
A C Q D G F S P F I S A L L H S L F V T P L Q P P D P S *

1201 AAGCTGAGCACAGACGAGCAGCTCCCTTCCAGCCCCCAGAAAGCTCGGTCACTTGAGTGTTCAGAAATCCTGGGGTGTCCCGGGCCGCTCTCA
1301 GAGAAAGTGGCAGGTTTCACGTTACGCGTGTGGCGGATCGTGTGGCTTCCAAAGCCTTTACAGCCCCCGCCCCCATCCCGTGGTCTGTCTGCAGGAAC
1401 TCTCCCGTCTGTGAGAAGCCTCTTTCCGAGTCGACCTCCCGGCCACCCCGCCCTGTGCTGTCTGGAAGAGCTCACTGCCAGCTGCGGCCTGGGCACCG
1501 CCGGCCATGTGTGTTTGCATGAGGAATCTTTAGTGGCAGACACCTAAGAGACGGCTGCGGTCACTCCAGCCTCCACCTCAATTTCTGTGTCCTCGGACTGAGAGCCA
1601 CATAGGACCAAGTTTCTGTGACTTTCTCAGTTGGCATGTTGACAGACATGTTTCCCTCTCCACCTCAATTTCTGTGTCCTCGGACTGAGAGCCA
1701 GGGGCGACATCATGACCTTCTGTCCCGCCGCTTAGCCCGGGAACAGGGAAGGAGCTGGGCCGTTTCTGTCTGTGTCCCATCCTGCTGCTCTCTGT
1801 CCTGGAATGTTTCAATGGGCCCGGGCCCCCAGGGAAGTTACCTCTGTGTGGTGGAGGCCACGGGACACCTCAGGTGCCACCCACCTTGGCCCTA
1901 AAACAGCCACCAAGGAAGCAGCCGAGAGCCGGACAGCGGGCAGCCTGTCTGGTTCTGTAGGCCCTGGGGTGGCAGACGAAACCCACGGCCCGTGTCC
2001 CAGCAGCAGGGTTGTCACTCGGAGCATCTGGGCTCCTGGCCGCTGTGTAGGTAGGNGCAGTACCGTGTATCGTAGGTAGCAGTAGGAACG
2101 GGGGCCACCGCGGCCCTGCAGCCGTTTCATGGCGGTGAGGTGTGTGCCAAGCCCCACCGGGGTGCAGGGCGTGACCGTGGGAATAAATAGGCGTTGTGA
2201 CCTCAAAAAAAAAAAAAAAA

FIG. 1B

FIG. 2A

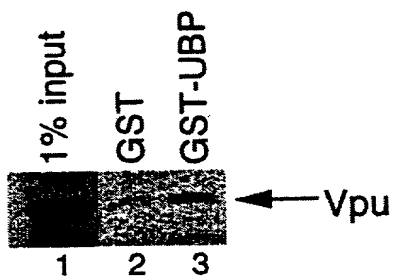


FIG. 2B

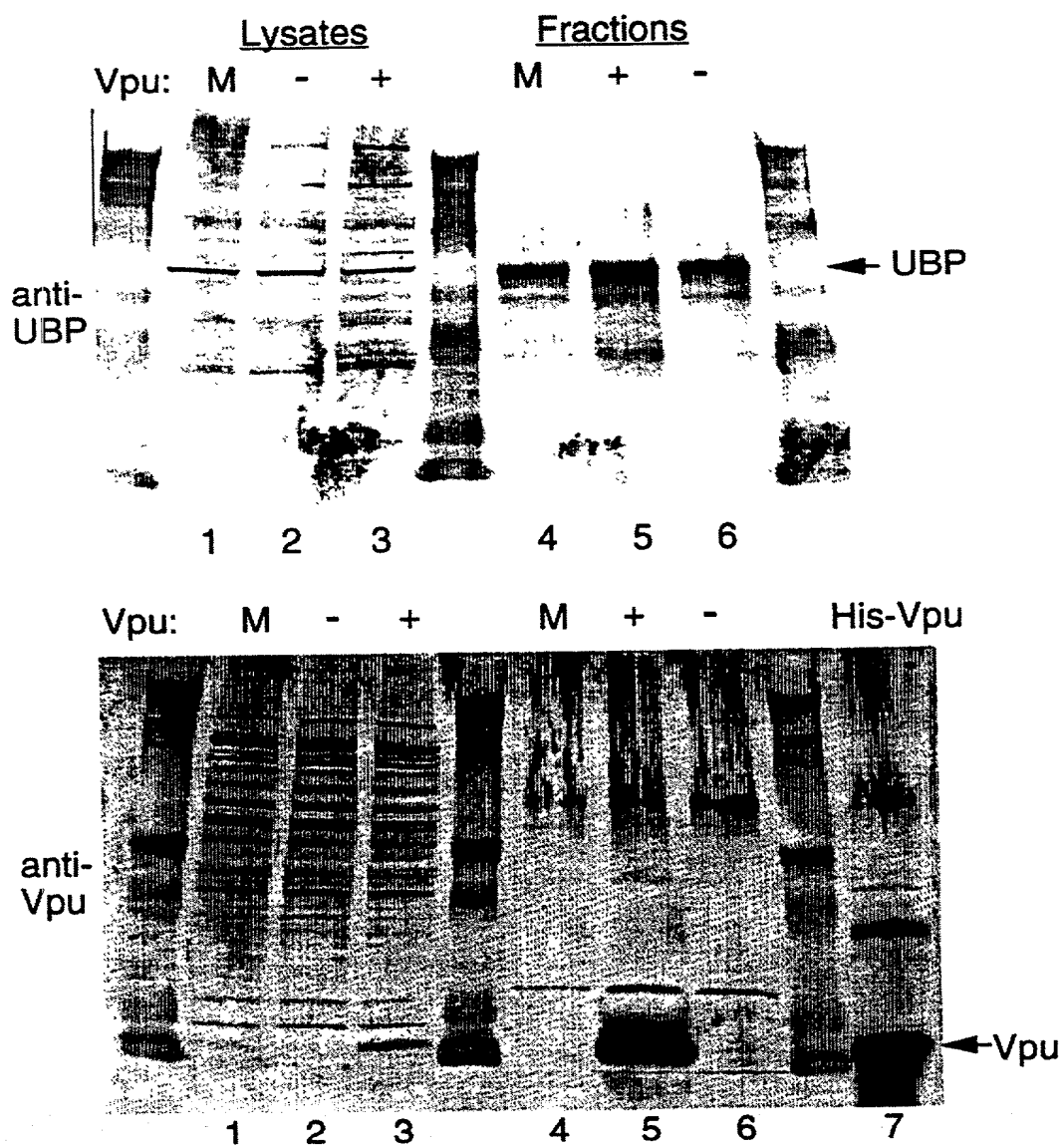


FIG 3A

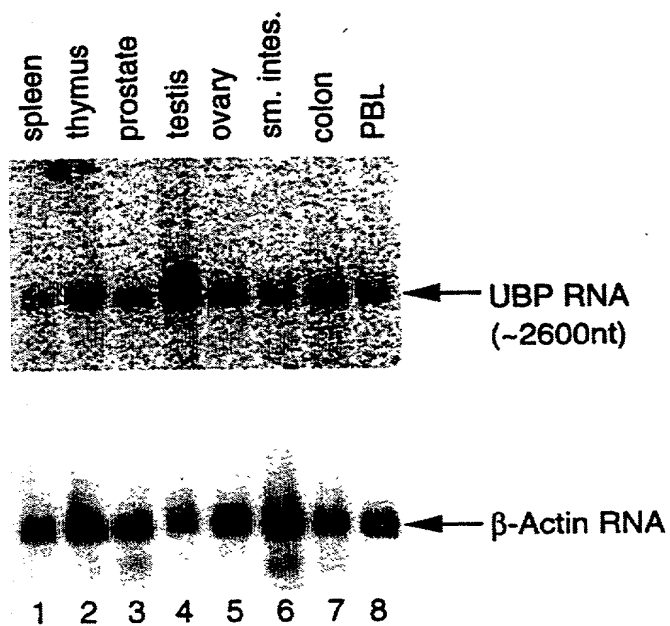


FIG 3B

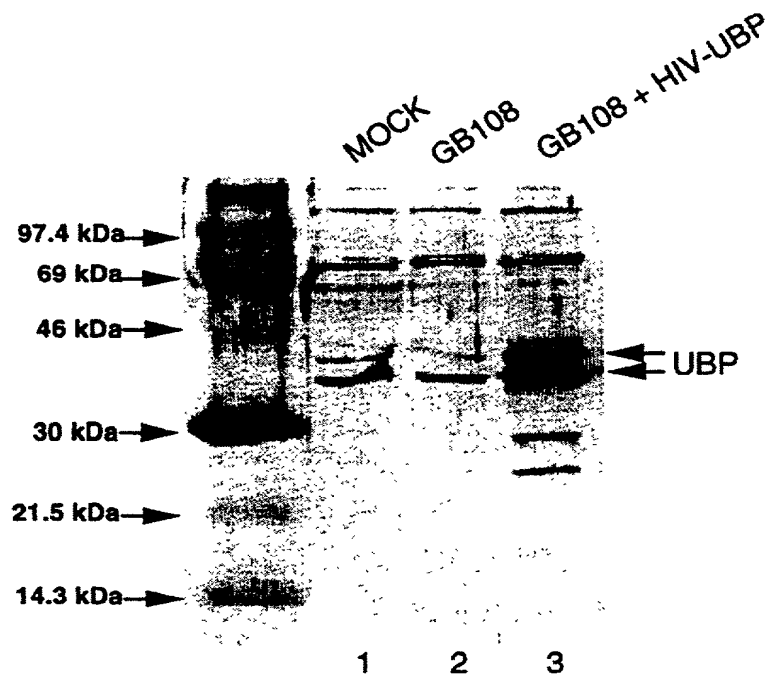
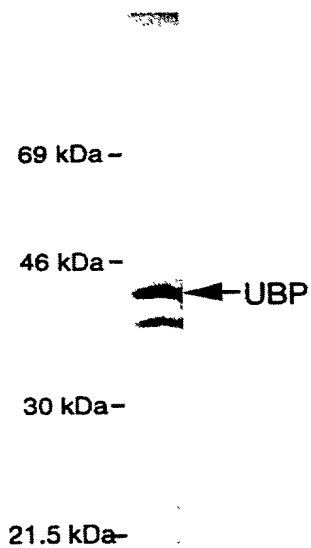


FIG 3C

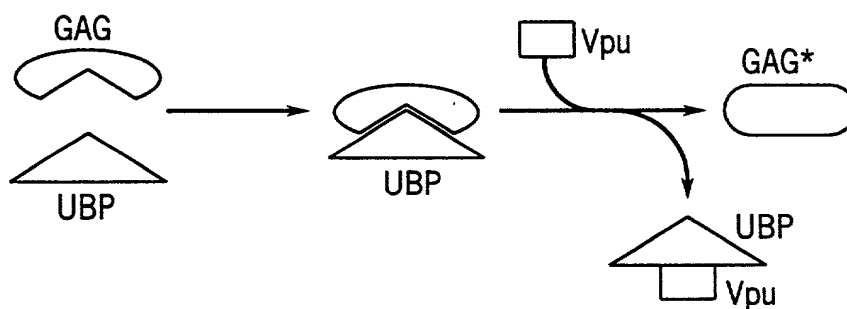
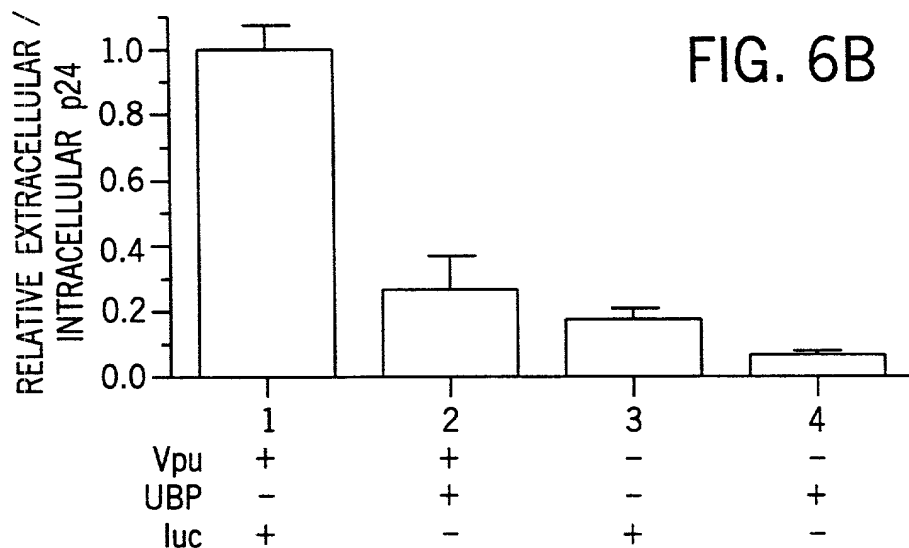
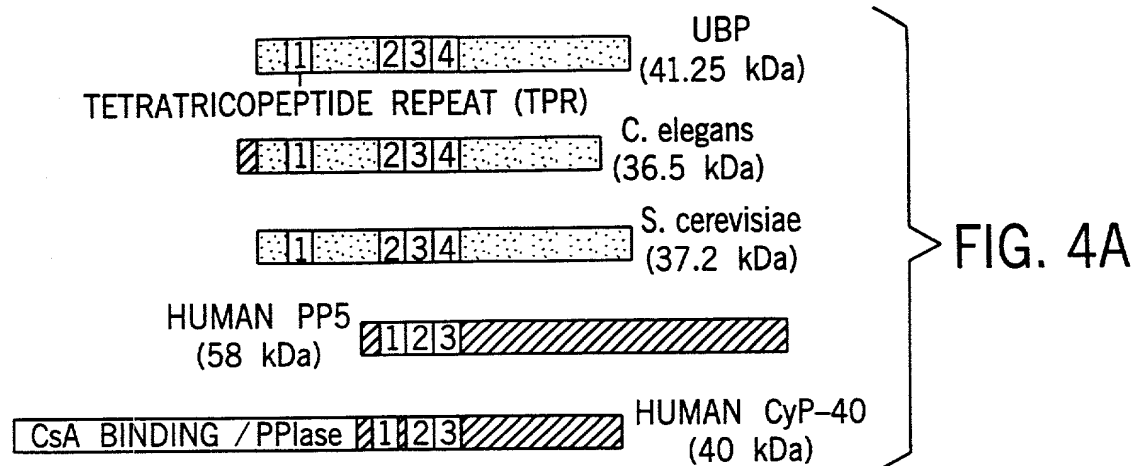


FIG. 4B

UBP	L	R	H	G	G	L	S	S	D	A	Q	E	S	L	E	V	A	I	Q	C	L	E	T	A	F	G	V	T	V	E	D	S	D	L	TPRL (19-52)
C. eleg.	V	S	Q	N	Q	A	T	A	E	Q	A	E	A	L	E	V	A	I	Q	C	L	E	H	S	F	G	L	D	D	A	S	Y	A	F	TPRL (38-71)
Scarev.	V	E	K	E	T	S	E	D	G	A	D	S	L	N	V	A	M	D	C	I	S	E	A	F	G	F	E	R	E	A	V	S	G	TPRL (20-53)	

UBP	L	K	T	E	G	N	E	Q	M	K	V	E	N	F	E	A	A	V	H	F	Y	G	K	A	I	E	L	N	P	A	N	A	V	TPR2 (94-127)	
C. eleg.	L	K	E	E	G	N	D	L	M	K	A	S	Q	F	E	A	A	V	Q	K	Y	N	A	A	I	K	L	N	R	D	P	.	V	Y	TPR2 (108-140)
S. cerev.	L	K	M	Q	G	N	K	A	M	A	N	K	D	Y	E	L	A	I	N	K	Y	T	E	A	I	K	V	L	P	T	N	A	I	Y	TPR2 (105-138)
ppp5	L	K	T	Q	A	N	D	Y	F	K	A	K	D	Y	E	N	A	I	K	F	Y	S	Q	A	I	E	L	N	P	S	N	A	I	Y	TPR1 (25-58)
Qp-40	L	K	N	I	G	N	T	F	F	K	S	Q	N	W	E	M	A	I	K	K	Y	A	E	V	L	R	Y	V	D	S	S	K	A	V	TPR1 (226-259)

UBP	F	C	N	R	A	A	A	Y	S	K	L	G	N	Y	A	G	A	V	Q	D	C	E	R	A	I	C	I	D	P	A	Y	S	K	A	TPR3 (128-161)
C. eleg.	F	C	N	R	A	A	A	Y	C	R	L	E	Q	Y	D	L	A	I	Q	D	C	R	T	A	L	A	L	D	P	S	Y	S	K	A	TPR3 (141-174)
S. cerev.	Y	A	N	R	A	A	A	H	S	S	L	K	E	Y	D	Q	A	V	K	D	A	E	S	A	I	S	I	D	P	S	Y	F	R	G	TPR3 (139-172)
pp5	Y	G	N	R	S	L	A	Y	L	R	T	E	C	Y	G	Y	A	L	G	D	A	T	R	A	I	E	L	D	K	K	Y	I	K	G	TPR2 (59-92)
OP40	V	L	N	I	G	A	C	K	L	K	M	S	N	W	Q	G	A	I	D	S	C	L	E	A	L	E	L	D	P	S	N	T	K	A	TPR2 (276-309)

UBBP	Y	G	R	M	G	L	A	L	S	S	L	N	K	H	V	E	A	V	A	Y	Y	K	K	A	L	E	L	D	P	D	N	E	T	Y	TPR4 (162-195)
C. eleg.	W	G	R	M	G	L	A	Y	S	C	Q	N	R	Y	E	H	A	A	E	A	Y	K	K	A	L	E	L	E	P	N	Q	E	S	Y	TPR4 (175-208)
S. cerev.	Y	S	R	L	G	F	A	K	Y	A	Q	G	K	P	E	E	A	L	E	A	Y	K	K	V	L	D	I	E	G	D	N	A	T	E	TPR4 (173-206)
pp5	Y	Y	R	R	A	A	S	N	M	A	L	G	K	F	R	A	A	L	R	D	Y	E	T	V	V	K	V	K	P	H	D	K	D	A	TPR3 (93-126)
Qp-40	L	Y	R	R	A	Q	G	W	Q	G	L	K	E	Y	D	Q	A	L	A	D	L	K	K	A	Q	G	I	A	P	E	D	K	A	I	TPR3 (310-343)

FIG. 5A

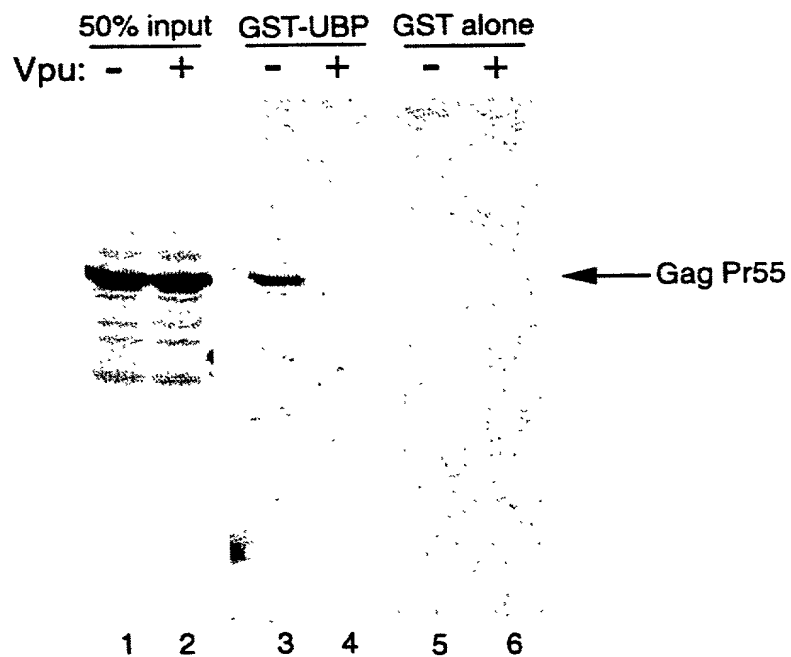
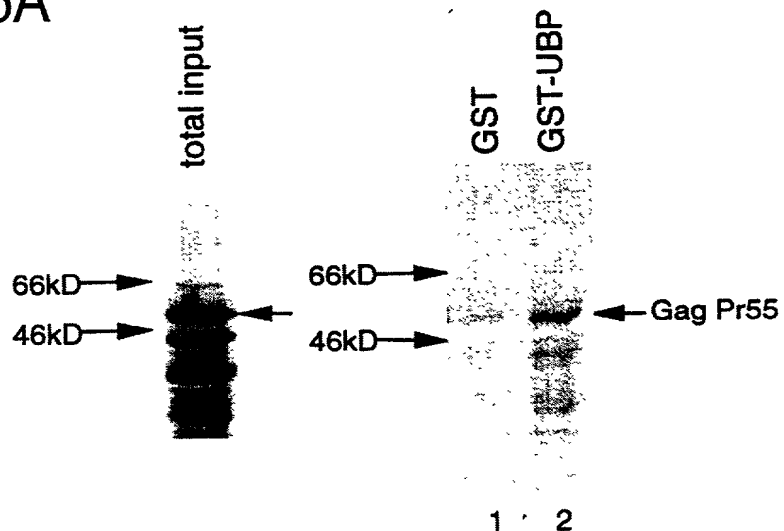


FIG. 5B

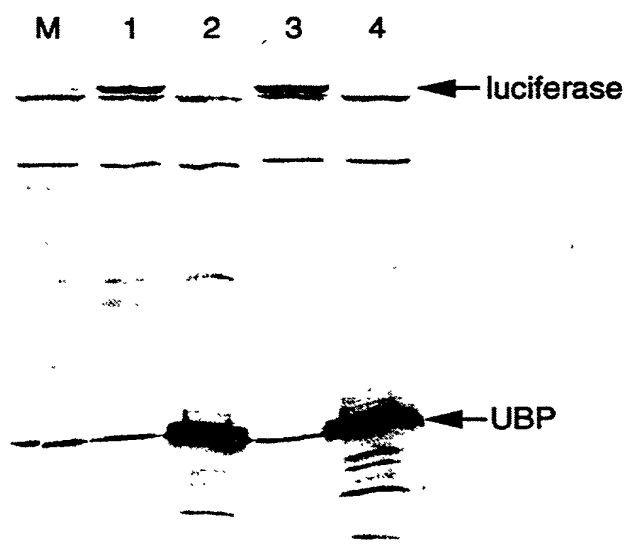


FIG. 6A